

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,653

DATE: 11/13/2001

TIME: 13:39:38

Input Set : A:\Is4367.txt

Output Set: N:\CRF3\11132001\I729653.raw

ENTERED

```

4 <110> APPLICANT: Lin, Biaoyang
6 <120> TITLE OF INVENTION: Prostate-Specific Polypeptide PAMP and
7   Encoding Nucleic Acid Molecules
10 <130> FILE REFERENCE: P-IS 4367
12 <140> CURRENT APPLICATION NUMBER: US 09/729,653
13 <141> CURRENT FILING DATE: 2000-12-04
15 <160> NUMBER OF SEQ ID NOS: 10
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 4500
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapien
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)...(4146)
28 <221> NAME/KEY: misc_feature
29 <222> LOCATION: (1)...(4500)✓
30 <223> OTHER INFORMATION: Xaa=any amino acid
32 <400> SEQUENCE: 1
33 cac tcg ctg att ggt cgc tgc tcg cgc ggt ctc ctg ggt gac ggg aac 48
34 His Ser Leu Ile Gly Arg Cys Ser Arg Gly Leu Leu Gly Asp Gly Asn
35 1 5 10 15
37 gcg gta gcc tgc ttg gtg gag acc ggg tgc gcc tgc gta ctt cat agt 96
38 Ala Val Ala Cys Leu Val Glu Thr Gly Cys Ala Cys Val Leu His Ser
39 20 25 30
41 tcg cgt agc ggc tcg agc gtg gag atg aag cgt att ttc tca ctg cta 144
42 Ser Arg Ser Gly Ser Ser Val Glu Met Lys Arg Ile Phe Ser Leu Leu
43 35 40 45
45 gaa aag act tgg ctt ggc gca cca ata cag ttt gcc tgg caa aaa aca 192
46 Glu Lys Thr Trp Leu Gly Ala Pro Ile Gln Phe Ala Trp Gln Lys Thr
47 50 55 60
49 tca gga aac tac ctt gca gta aca gga gct gat tat att gtg aaa atc 240
50 Ser Gly Asn Tyr Leu Ala Val Thr Gly Ala Asp Tyr Ile Val Lys Ile
51 65 70 75 80
53 ttt gat cgc cat ggt caa aaa aga agt gaa att aac tta cct ggt aac 288
54 Phe Asp Arg His Gly Gln Lys Arg Ser Glu Ile Asn Leu Pro Gly Asn
55 85 90 95
57 tgt gtt gcc atg gat tgg gat aaa gat gga gat gtc cta gca gtg att 336
58 Cys Val Ala Met Asp Trp Asp Lys Asp Gly Asp Val Leu Ala Val Ile
59 100 105 110
61 gct gag aaa tct agc tgc att tat ctt tgg gat gcc aac aca aat aag 384
62 Ala Glu Lys Ser Ser Cys Ile Tyr Leu Trp Asp Ala Asn Thr Asn Lys
63 115 120 125
65 acc agc cag tta gac aat ggc atg agg gat caa atg tct ttc ctt ctt 432
66 Thr Ser Gln Leu Asp Asn Gly Met Arg Asp Gln Met Ser Phe Leu Leu
67 130 135 140
69 tgg tca aaa gtt gga agt ttc ctg gct gtt gga act gtt aaa gga aat 480

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70 Trp Ser Lys Val Gly Ser Phe Leu Ala Val Gly Thr Val Lys Gly Asn  
 71 145 150 155 160  
 73 ttg stt att tat aat cat cag aca tct cga aag att cct gtc ctt gga 528  
 W--> 74 Leu Xaa Ile Tyr Asn His Gln Thr Ser Arg Lys Ile Pro Val Leu Gly  
 75 165 170 175  
 77 aaa cat act aag aga atc act tgt gga tgt tgg aat gca gaa aat ctg 576  
 78 Lys His Thr Lys Arg Ile Thr Cys Gly Cys Trp Asn Ala Glu Asn Leu  
 79 180 185 190  
 81 cyt gct tta ggt ggt gaa gat aaa atg att aca gtt agt aat cag gaa 624  
 W--> 82 Xaa Ala Leu Gly Gly Glu Asp Lys Met Ile Thr Val Ser Asn Gln Glu  
 83 195 200 205  
 85 ggt gac acg ata aga cag aca caa gtg aga tca gag cct akc aac atg 672  
 W--> 86 Gly Asp Thr Ile Arg Gln Thr Gln Val Arg Ser Glu Pro Xaa Asn Met  
 87 210 215 220  
 89 cag ttt ttc ttg atg aag atg gat gac cga acc tct gct gct gaa agc 720  
 90 Gln Phe Phe Leu Met Lys Met Asp Asp Arg Thr Ser Ala Ala Glu Ser  
 91 225 230 235 240  
 93 atg ata agt gtg gtg ctt ggc aag aaa act ttg ttt tta aat ctg 768  
 94 Met Ile Ser Val Val Leu Gly Lys Lys Thr Leu Phe Phe Leu Asn Leu  
 95 245 250 255  
 97 aat gaa cca gat aac cca gct gat ctt gaa ttt cag cag gac ttt ggc 816  
 98 Asn Glu Pro Asp Asn Pro Ala Asp Leu Glu Phe Gln Gln Asp Phe Gly  
 99 260 265 270  
 101 aac att gtc tgc tat aat tgg tat ggt gat ggc cgc atc atg att ggt 864  
 102 Asn Ile Val Cys Tyr Asn Trp Tyr Gly Asp Gly Arg Ile Met Ile Gly  
 103 275 280 285  
 105 ttt tca tgt gga cat ttt gtg gtc att tct act cat act gga gag ctt 912  
 106 Phe Ser Cys Gly His Phe Val Val Ile Ser Thr His Thr Gly Glu Leu  
 107 290 295 300  
 109 ggt caa gag ata ttt cag gct cgt aac cat aaa gat aat cta acc agc 960  
 110 Gly Gln Glu Ile Phe Gln Ala Arg Asn His Lys Asp Asn Leu Thr Ser  
 111 305 310 315 320  
 113 att gca gta tca cag act ctt aac aaa gtt gct aca tgt gga gat aac 1008  
 114 Ile Ala Val Ser Gln Thr Leu Asn Lys Val Ala Thr Cys Gly Asp Asn  
 115 325 330 335  
 117 tgc att aaa atc caa gac ttg gtt gac tta aaa gac atg tat gtt ata 1056  
 118 Cys Ile Lys Ile Gln Asp Leu Val Asp Leu Lys Asp Met Tyr Val Ile  
 119 340 345 350  
 121 ctc aac ctg gat gag gaa aat aaa gga ttg ggt acc ttg tcc tgg act 1104  
 122 Leu Asn Leu Asp Glu Glu Asn Lys Gly Leu Gly Thr Leu Ser Trp Thr  
 123 355 360 365  
 125 gat gat ggc cag ttg cta gca ctc tct acc caa agg ggc tca ctt cat 1152  
 126 Asp Asp Gly Gln Leu Leu Ala Leu Ser Thr Gln Arg Gly Ser Leu His  
 127 370 375 380  
 129 gtt ttc ctg acc aag ctt ccc ata ctt ggg gat gcc tgc agc aca agg 1200  
 130 Val Phe Leu Thr Lys Leu Pro Ile Leu Gly Asp Ala Cys Ser Thr Arg  
 131 385 390 395 400  
 133 att gcc tat ctc acc tcc ctc ctt gaa gtc acc gta gcc aac cct gtt 1248  
 134 Ile Ala Tyr Leu Thr Ser Leu Leu Glu Val Thr Val Ala Asn Pro Val

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135		405		410		415		
137	gaa gga gag	cta cca atc	aca gtt tct	gtt gat gtg	gaa ccc aac	ttt	1296	
138	Glu Gly Glu	Leu Pro Ile	Thr Val Ser	Val Asp Val	Glu Pro Asn	Phe		
139		420		425		430		
141	gtg gca gta	ggt ctt tat	cat ctg gct	gta gga atg	aat aat cga	gct	1344	
142	Val Ala Val	Gly Leu Tyr	His Leu Ala	Val Gly Met	Asn Asn Arg	Ala		
143		435		440		445		
145	tgg ttt tat	gtc ctt gga	gaa aat gct	gtg aaa aaa	ttg aaa gat	atg	1392	
146	Trp Phe Tyr	Val Leu Gly	Glu Asn Ala	Val Lys Lys	Leu Lys Asp	Met		
147		450		455		460		
149	gag tat ctg	gga aca gta	gcc agt att	tgc ctt cat	tct gac tat	gct	1440	
150	Glu Tyr Leu	Gly Thr Val	Ala Ser Ile	Cys Leu His	Ser Asp Tyr	Ala		
151	465		470		475	480		
153	gct gca ctt	ttt gaa ggc	aaa gtc cag	tta cat ttg	ata gaa agc	gaa	1488	
154	Ala Ala Leu	Phe Glu Gly	Lys Val Gln	Leu His Leu	Ile Glu Ser	Glu		
155		485		490		495		
157	atc ttg gat	gct caa gaa	gaa cgt gag	act cgg ctt	ttc cca gca	gtg	1536	
158	Ile Leu Asp	Ala Gln Glu	Glu Arg Glu	Thr Arg Leu	Phe Pro Ala	Val		
159		500		505		510		
161	gat gat aag	tgc cgt atc	tta tgc cat	gcc tta act	agt gat ttc	ctc	1584	
162	Asp Asp Lys	Cys Arg Ile	Leu Cys His	Ala Leu Thr	Ser Asp Phe	Leu		
163		515		520		525		
165	atc tat ggt	aca gat act	ggt gtc gtt	cag tat ttc	tac att gaa	gac	1632	
166	Ile Tyr Gly	Thr Asp Thr	Gly Val Val	Gln Tyr Phe	Tyr Ile Glu	Asp		
167		530		535		540		
169	tgg caa ttc	gtt aat gat	tat cga cat	cct gtc agt	gtg aaa aag	att	1680	
170	Trp Gln Phe	Val Asn Asp	Tyr Arg His	Pro Val Ser	Val Lys Lys	Ile		
171	545		550		555	560		
173	ttt ccc gac	cca aat ggg	acc aga tta	gtt ttc att	gat gaa aaa	agt	1728	
174	Phe Pro Asp	Pro Asn Gly	Thr Arg Leu	Val Phe Ile	Asp Glu Lys	Ser		
175		565		570		575		
177	gat gga ttt	gtt tac tgt	cca gtc aat	gac gct acc	tat gag att	cca	1776	
178	Asp Gly Phe	Val Tyr Cys	Pro Val Asn	Ala Thr Tyr	Glu Ile Pro			
179		580		585		590		
181	gat ttt tca	cca acc att	aaa ggt gtt	ctt tgg gaa	aac tgg cca	atg	1824	
182	Asp Phe Ser	Pro Thr Ile	Lys Gly Val	Leu Trp Glu	Asn Trp Pro	Met		
183		595		600		605		
185	gat aaa ggt	gta ttt att	gct tat gat	gat gat aag	gtg tac act	tat	1872	
186	Asp Lys Gly	Val Phe Ile	Ala Tyr Asp	Asp Asp Lys	Val Tyr Thr	Tyr		
187		610		615		620		
189	gtc ttt cac	aag gac act	ata caa gga	gcc aag gtt	att ttg gct	ggt	1920	
190	Val Phe His	Lys Asp Thr	Ile Gln Gly	Ala Lys Val	Ile Leu Ala	Gly		
191	625		630		635	640		
193	agc acc aaa	gtt cct ttt	gct cat aaa	cct ttg ctg	cta tat aat	gga	1968	
194	Ser Thr Lys	Val Pro Phe	Ala His Lys	Pro Leu Leu	Leu Tyr Asn	Gly		
195		645		650		655		
197	gag ctg acc	tgc caa aca	cag agt gga	aaa gta aac	aac atc tac	ctt	2016	
198	Glu Leu Thr	Cys Gln Thr	Gln Ser Gly	Lys Val Asn	Asn Ile Tyr	Leu		
199		660		665		670		

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```

201 agc acc cat ggc ttt ctc agc aac tta aaa gat asg ggg cct gac gaa 2064
W--> 202 Ser Thr His Gly Phe Leu Ser Asn Leu Lys Asp Xaa Gly Pro Asp Glu
203          675          680          685
205 ctg aga cca atg ctg gca cac aat tta atg cta aag agg ttt tct gat 2112
206 Leu Arg Pro Met Leu Ala His Asn Leu Met Leu Lys Arg Phe Ser Asp
207          690          695          700
209 gct tgg gaa atg tgc agg att ctg aat gat gag gct gcc tgg aat gag 2160
210 Ala Trp Glu Met Cys Arg Ile Leu Asn Asp Glu Ala Ala Trp Asn Glu
211 705          710          715          720
213 ttg gcc aga gct tgt cta cat cac atg gaa gtg gag ttt gca atc cgt 2208
214 Leu Ala Arg Ala Cys Leu His His Met Glu Val Glu Phe Ala Ile Arg
215          725          730          735
217 gtt tat cgg aga att gga aat gtt ggc ata gtg atg tcc ttg gaa caa 2256
218 Val Tyr Arg Arg Ile Gly Asn Val Gly Ile Val Met Ser Leu Glu Gln
219          740          745          750
221 ata aag gga ata gag gac tac aat ctt ttg gca gga cac ctt gcc atg 2304
222 Ile Lys Gly Ile Glu Asp Tyr Asn Leu Leu Ala Gly His Leu Ala Met
223          755          760          765
225 ttt acc aac gat tat aac ctg gct cag gac ttg tac ctt gca tcc agc 2352
226 Phe Thr Asn Asp Tyr Asn Leu Ala Gln Asp Leu Tyr Leu Ala Ser Ser
227          770          775          780
229 tgt cct att gct gcc ctg gag atg aga agg gat tta cag cat tgg gac 2400
230 Cys Pro Ile Ala Ala Leu Glu Met Arg Arg Asp Leu Gln His Trp Asp
231 785          790          795          800
233 agt gct cta caa ctg gca aag cat ttg gcc cca gac cag ata cct ttt 2448
234 Ser Ala Leu Gln Leu Ala Lys His Leu Ala Pro Asp Gln Ile Pro Phe
235          805          810          815
237 ata tca aaa gaa tat gct att cag ctt gaa ttc gcg ggt gat tat gta 2496
238 Ile Ser Lys Glu Tyr Ala Ile Gln Leu Glu Phe Ala Gly Asp Tyr Val
239          820          825          830
241 aat gct ttg gct cat tat gag aaa gga ata aca ggt gat aat aag gaa 2544
242 Asn Ala Leu Ala His Tyr Glu Lys Gly Ile Thr Gly Asp Asn Lys Glu
243          835          840          845
245 cat gat gaa gct tgt ctg gct gga gtg gcc cag atg tcc ata aga atg 2592
246 His Asp Glu Ala Cys Leu Ala Gly Val Ala Gln Met Ser Ile Arg Met
247          850          855          860
249 gga gac ata cgt cga ggg gtt aac caa gcc ctc aag cat ccc agc agg 2640
250 Gly Asp Ile Arg Arg Gly Val Asn Gln Ala Leu Lys His Pro Ser Arg
251 865          870          875          880
253 gtc ctt aaa aga gac tgt gga gcc ata ttg gag aat atg aag caa ttt 2688
254 Val Leu Lys Arg Asp Cys Gly Ala Ile Leu Glu Asn Met Lys Gln Phe
255          885          890          895
257 tca gaa gcg gcc caa ctg tat gaa aaa ggt ctc tac tac gat aaa gca 2736
258 Ser Glu Ala Ala Gln Leu Tyr Glu Lys Gly Leu Tyr Tyr Asp Lys Ala
259          900          905          910
261 gca tct gtt tac atc cgc tct aag aat tgg gca aaa gtt ggt gat ctt 2784
262 Ala Ser Val Tyr Ile Arg Ser Lys Asn Trp Ala Lys Val Gly Asp Leu
263          915          920          925
265 ctg ccc cac gtt tct tct cct aag atc cat ttg cag tat gcc aaa gcc 2832

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```

266 Leu Pro His Val Ser Ser Pro Lys Ile His Leu Gln Tyr Ala Lys Ala
267      930      935      940
269 aag gaa gca gat gga aga tac aaa gaa gct gtt gta gct tat gaa aat 2880
270 Lys Glu Ala Asp Gly Arg Tyr Lys Glu Ala Val Val Ala Tyr Glu Asn
271 945      950      955      960
273 gca aaa cag tgg caa agt gta atc cgc atc tat ctg gat cac ctc aat 2928
274 Ala Lys Gln Trp Gln Ser Val Ile Arg Ile Tyr Leu Asp His Leu Asn
275      965      970      975
277 aat cct gaa aaa gct gtc aat att gtt aga gag acc cag tct ctg gat 2976
278 Asn Pro Glu Lys Ala Val Asn Ile Val Arg Glu Thr Gln Ser Leu Asp
279      980      985      990
281 gga gcc aaa atg gta gcc agg ttt ttt cta cag ctt ggt gac tat ggg 3024
282 Gly Ala Lys Met Val Ala Arg Phe Phe Leu Gln Leu Gly Asp Tyr Gly
283      995      1000      1005
285 tct gcc atc cag ttt ctt gtc atg tcc aaa tgc aac aat gaa gct ttc 3072
286 Ser Ala Ile Gln Phe Leu Val Met Ser Lys Cys Asn Asn Glu Ala Phe
287 1010      1015      1020
289 aca ctg gct cag caa cac aac aaa atg gaa atc tat gca gat att att 3120
290 Thr Leu Ala Gln Gln His Asn Lys Met Glu Ile Tyr Ala Asp Ile Ile
291 1025      1030      1035      1040
293 ggt tct gaa gac act act aat gaa gac tat caa agc att gcc tta tac 3168
294 Gly Ser Glu Asp Thr Thr Asn Glu Asp Tyr Gln Ser Ile Ala Leu Tyr
295      1045      1050      1055
297 ttt gaa gga gaa aag aga tat ctt cag gct gga aaa ttc ttc ttg ctg 3216
298 Phe Glu Gly Glu Lys Arg Tyr Leu Gln Ala Gly Lys Phe Phe Leu Leu
299      1060      1065      1070
301 tgt ggc caa tat tca cga gca ctt aaa cac ttc ctg aaa tgc cca agc 3264
302 Cys Gly Gln Tyr Ser Arg Ala Leu Lys His Phe Leu Lys Cys Pro Ser
303      1075      1080      1085
305 tcg gaa gat aat gtg gca ata gaa atg gca att gaa act gtt ggt cag 3312
306 Ser Glu Asp Asn Val Ala Ile Glu Met Ala Ile Glu Thr Val Gly Gln
307 1090      1095      1100
309 gcc aaa gat gaa ctg ctg acc aat cag ctg ata gac cat ctc ctg ggg 3360
310 Ala Lys Asp Glu Leu Leu Thr Asn Gln Leu Ile Asp His Leu Leu Gly
311 1105      1110      1115      1120
313 gag aac gat ggc atg cct aag gat gcc aag tac ctg ttc cgc ttg tac 3408
314 Glu Asn Asp Gly Met Pro Lys Asp Ala Lys Tyr Leu Phe Arg Leu Tyr
315      1125      1130      1135
317 atg gct ctg aag caa tac cga gaa gct gcc cag act gcc atc atc att 3456
318 Met Ala Leu Lys Gln Tyr Arg Glu Ala Ala Gln Thr Ala Ile Ile Ile
319      1140      1145      1150
321 gcc aga gaa gag cag tct gca ggc aac tac cgg aat gca cac gat gtt 3504
322 Ala Arg Glu Glu Gln Ser Ala Gly Asn Tyr Arg Asn Ala His Asp Val
323      1155      1160      1165
325 ctc ttc agt atg tat gca gaa ctg aaa tcc cag aag atc aaa att ccc 3552
326 Leu Phe Ser Met Tyr Ala Glu Leu Lys Ser Gln Lys Ile Lys Ile Pro
327 1170      1175      1180
329 tcc gag atg gcc acc aac ctc atg att ctg cac agc tat ata cta gta 3600
330 Ser Glu Met Ala Thr Asn Leu Met Ile Leu His Ser Tyr Ile Leu Val

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L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2